

us-10-046-433-39.rng

Wed Mar 12 10:08:32 2003

GenCore version 5.1.4.p5, 4/5/03
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IDEAS/NUC search, using sw model

OM nucleic - nucleic search, using sw model
Run on: March 11, 2003, 03:27:47 ; Search time 490 seconds
(without alignments) 11 updates/sec
15322.780 Million cell

title: US-10-046-433-39
perfect score: 334
sequence: 1 gcaagaaggcggcggcagg... attaaaaaaaaaaaaaaa 3334

scoring table: 1DEAS/NUC
gapop 10.0 , Gapext 1.0
2185239 seqs, 1125999159 residues

Searched: 4370478 hits satisfying chosen parameters:

Total number of hits length: 0
Minimum DB seq length: 2000000000
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT: *
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002B.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002C.DAT: *
24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002D.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score distribution and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3334	100.0	3334	22	AAP28030 Human TR13 receptor
2	3333.4	99.8	3331	22	AAS21262 Human cDNA sequence
3	3299.6	97.8	3280	21	AAP55442 Human CASB19 protein
4	3258.8	97.2	3273	22	AAPF89774 Nucleotide sequence
5	2726.6	81.8	2610	22	AAP27997 Human TR13 receptor
6	2603.6	78.1	2554	22	AAP21991 Human endometrial
7	2527.4	75.8	1717	20	AAP21991 Human prostate
8	1705	51.1	1299	23	ABV23150 Human prostate
9	1172.8	35.2			

XX
 PT Nucleic acids encoding 2 human tumor necrosis factor receptor
 PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
 PT and treatment of, e.g., cancers, acquired immune deficiency syndrome and
 XX
 PS Claim 4: Page 394-398; 418pp; English.
 The present invention provides the protein and coding sequences of the
 human tumor necrosis factor receptors TR13 and TR14. These sequences are
 useful in the diagnosis and treatment of many diseases, including cancer,
 autoimmune diseases, neurodegenerative diseases, graft rejection, allergies,
 neurodegenerative diseases, grant rejection, inflammation, aneurysms and
 XX
 Sequence 334 BP; 820 A; 952 C; 811 G; 751 T; 0 other;
 Best Local Similarity 100.0%; Score 334;
 Matches 334; Conservative 100.0%; Pred. No: 0;
 QY 1 GCAGAAAGAGCAGACCTGAGGAGACTGAGCGCTACTGAGGAGACCTGAG 840
 Db 1 GCAGAAACGACAGCAGCGACGACCTGAGGAGACTGAGCGCTACTGAGGAG 840
 QY 61 GCTGAGCCTGGGACACSCACCATCTCCGCGAGCTGGGAGACTGAGGAGC 60
 Db 61 GCTGAGCCTGGGACACSCACCATCTCCGCGAGCTGGGAGACTGAGGAGC 60
 QY 121 ATACCCGGCGCTGGCGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 120
 Db 121 ATACCCGGCGCTGGCGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 120
 QY 181 AGGGACGCCGAGGCTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 180
 Db 181 AGGGACGCCGAGGCTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 180
 QY 241 GACGACCGGGCTCAGGGAGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 240
 Db 241 GACGACCGGGCTCAGGGAGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 240
 QY 301 CTGGCAGGCCCTCAAGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 300
 Db 301 CTGGCAGGCCCTCAAGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 300
 QY 361 GATATGAGGAGGACCTGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 360
 Db 361 GATATGAGGAGGACCTGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 360
 QY 421 ATTCGGTGTGAGCTGGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 420
 Db 421 ATTCGGTGTGAGCTGGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 420
 QY 481 GAGCTGAGTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 480
 Db 481 GAGCTGAGTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 480
 QY 541 CGGGCGACTACCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 540
 Db 541 CGGGCGACTACCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 540
 QY 601 AACCTGAGAAGTGGACCTTACTCTGAACTGACCTGGCGCTGGCGCTGGCGCTGGCG 600
 Db 601 AACCTGAGAAGTGGACCTTACTCTGAACTGACCTGGCGCTGGCGCTGGCGCTGGCG 600
 QY 661 TTGGATTTGGCTGAGTAACTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 660
 Db 661 TTGGATTTGGCTGAGTAACTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 660
 QY 721 AGGACACAGAGAAGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 720
 Db 721 AGGACACAGAGAAGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 720
 QY 780 GAGGAGACACTACGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 780
 Db 780 GAGGAGACACTACGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 780
 QY 781 CTCATATGGAGAACCCGCTCTGAGTGGACCAAGCTTCTCCCTGAGCTGGCG 780
 Db 781 CTCATATGGAGAACCCGCTCTGAGTGGACCAAGCTTCTCCCTGAGCTGGCG 780
 QY 841 AGAACACTGGCTACAGGCTCTCTGAGCTGGCGCTGGCGCTGGCGCTGGCG 840
 Db 841 AGAACACTGGCTACAGGCTCTCTGAGCTGGCGCTGGCGCTGGCGCTGGCG 840
 QY 901 AGCTACGAGACAGCAGGCTCTCTGAGCTGGCGCTGGCGCTGGCGCTGGCG 900
 Db 901 AGCTACGAGACAGCAGGCTCTCTGAGCTGGCGCTGGCGCTGGCGCTGGCG 900
 QY 961 AATAAAGAGAACTGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 960
 Db 961 AATAAAGAGAACTGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 960
 QY 1081 TCCATGGGAGAACCTCTGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1080
 Db 1081 TCCATGGGAGAACCTCTGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1080
 QY 1141 GAGGACCTGGGGAGTGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1140
 Db 1141 GAGGACCTGGGGAGTGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1140
 QY 1201 TCCACCCAGGCTTCACAAACACACACACACACACACACACACACACACACAC 1200
 Db 1201 TCCACCCAGGCTTCACAAACACACACACACACACACACACACACACACAC 1200
 QY 1261 TACTCCAAATGGCTCAGTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1260
 Db 1261 TACTCCAAATGGCTCAGTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1260
 QY 1321 GAAATACAAATGGGAGACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1320
 Db 1321 GAAATACAAATGGGAGACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1320
 QY 1381 AACCTGAGTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1380
 Db 1381 AACCTGAGTACGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1380
 QY 1441 GCTGGACCTCAGACATRACTCTGAGCTGGCGCTGGCGCTGGCGCTGGCG 1440
 Db 1441 GCTGGACCTCAGACATRACTCTGAGCTGGCGCTGGCGCTGGCGCTGGCG 1440
 QY 1501 CGCACTGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1500
 Db 1501 CGCACTGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1500
 QY 1561 GAGCCTCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1560
 Db 1561 GAGCCTCTGGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1560
 QY 1621 AACACTCCCTGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1620
 Db 1621 AACACTCCCTGGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1620
 QY 1681 GAGGAGACACTACGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1680
 Db 1681 GAGGAGACACTACGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1680
 QY 1741 AGCAGGAAGTACACGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1740
 Db 1741 AGCAGGAAGTACACGAGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1740
 QY 1801 AATGGCTCTGGCTCTACTCTGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1800
 Db 1801 AATGGCTCTGGCTCTACTCTGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1800
 QY 1861 TGCACCTCTGGCTCTACTCTGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 1860

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QY	598	GTCAACCTGAGCAATCTGGCACCGTTAACCTCGATACTACATCCAGTCAGCATC
Db	541	GTCACACCAGAAGACAACTGCGACCGTCACTCGATACTACATCCAGTCAGCATC
QY	658	ATCTTCAGTTTGTGTCAGATGAGATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	601	ACTTGTAGTTTGTGTCAGATGAGATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	718	ATGAGACACAGAGAGAGATGAGATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	661	ATGAGACACAGAGAGATGAGATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	778	GTCTCTATGGAGAACACACGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	721	GTCTCTATGGAGAACACACGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	838	GTGAGAACATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	781	GTGAGAACATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	898	GGACCTATCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG
Db	841	GGACCTATCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG
QY	958	TCAATAAGGAGAACTCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	901	TCAATAAGGAGAACTCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1018	TCTCTTCTCTGTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	961	TCTCTTCTCTGTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1078	GCCRGCGATGTCAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1021	GCCRGCGATGTCAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1138	ACGAGACCTTGAGGGCGAGTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1081	ACGAGACCTTGAGGGCGAGTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1198	CCCTGCACCCAGGCTCTTCAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1141	CCCTGCACCCAGGCTCTTCAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1258	TCTCTCTTCTCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1201	TCTCTCTTCTCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1318	TTGAAATCAATGGTGGAGACAGACGACGACGACGACGACGACGACGACGACGACG
Db	1261	TTGAAATCAATGGTGGAGACAGACGACGACGACGACGACGACGACGACGACGACG
QY	1378	ATCAACTTGAGTACAAGGAGATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1321	ATCAACTTGAGTACAAGGAGATGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1438	GTCTCTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1381	GTCTCTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1498	CCTGGCAGCTGGTGGAGCGACAGACGACGACGACGACGACGACGACGACGACGACG
Db	1441	CCTGGCAGCTGGTGGAGCGACAGACGACGACGACGACGACGACGACGACGACGACG
QY	1558	TTGAGACCCCTGTCGTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
Db	1501	TTTGGAGACCCCTGTCGTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1618	ACCAAGACTCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG
QY	1561	TTTGGAGACCCCTGTCGTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTGAGCTTG

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QY	1786	GCACCAATGATGAACTGGCTTCTACTGCCCTAGAACCCCT	1845	Db	2853	CTAGATCAGTACTCCAAAGTGATGATCTACTCTGAGACTSGACCTGCA	2912
Db	1773	GTCACCAATGATGAACTGGCTTCTACTGCCCTAGAACCCCT	1832	QY	2926	GCAGCTACACTTGCGCATCAGGAAGGGAGTGGAGACGACCTCATCTTAC	2985
QY	1846	GATGTGGCTCCCTGCACCTCTGTGCTGGTTACTATATGACCGAGATTCAGA	1905	Db	2913	GCAGCTACACTTGCGCATCAGGAAGGGAGTGGAGACGACCTCATCTTAC	2972
Db	1893	ACCTGCACTCTGTCGCCCTAACACAAATCTGAAAGCGATTCAGA	1892	QY	2986	AGCAGAA-TCACTCTGGAAAGTCATCAATTTACCTCAAGAGGACTCTGTGAGGA	3044
QY	1966	GCCTGTTGCTCTGGGCCAGGACAGAACAGACAGATCCTCTGTCAGA	1965	Db	2973	AGCAAGACTCTTGGAGAACATCAATCTTCAGAGGACCTGAGAGCA	3104
Db	1906	ACCTGCACTCTGTCGCCCTAACACAAATCTGAAAGCGATTCAGA	1952	QY	3045	TGTGACTCAGTGGCGAGAAGACATCTCAGAGGAGCCATGGTCCAG	3092
Db	2026	GATGCACTCTGTCGCCCTAACACAAATCTGAAAGCGATTCAGA	2025	Db	3033	TGTGACTCAGTGGCGAGAAGACATCTCAGAGGAGCCATGGTCCAG	3164
QY	2013	GATGCACTCTGTCGCCCTAACACAAATCTGAAAGCGATTCAGA	2012	QY	3105	CTGCTGCCTACCCGCGCTCTACCTCTGAGACCTTGAGACGCTGGGGA	3152
QY	2086	GCAACACCGTCACTCTGTCAGGAGCCAGCTCAACCAACGAGACTTCAGA	2085	Db	3093	CTGCTGCCTACCCGCGCTCTACCTCTGAGACCTTGAGACGCTGGGGA	3224
Db	2073	GCAACACCGTCACTCTGTCAGGAGCCAGCTCAACCAACGAGACTTCAGA	2072	QY	3165	GGTGCCAGCATCTGCACACCCACTGCTGGAATCTCTGTCGCTTACAGT	3212
QY	2146	CATCACTTACCTCTGTCCTCTGTCAGGAAACAGGTTAGGAAATGCTGACG	2145	Db	3153	GTTGCCAGCATCTGCACACCCACTGCTGTCAGACCTTGAGACCTTGAGC	3284
Db	2133	CATCACTTACCTCTGTCCTCTGTCAGGAAACAGGTTAGGAAATGCTGACG	2132	QY	3225	TTGAGATTGAGATCTTTATAGTGTGAAATTTAAAGAAAAAAAGA	3334
QY	2206	AATGTCAGTACCTCCGAGATCCGGATTCAGGGTTGACTCAGGGTCTCC	2252	Db	3213	TTGAGATTGAGATCTTTATAGTGTGAAATTTAAAGAAAAAAAGA	3322
Db	2193	AATGTCAGTACCTCCGAGATTCAGGGTTGACTCAGGGTCTCC	2325	QY	3285	CTGCAAAATAAACCAACATTGTTGTAATTTAAAGAAAAAAAGA	3322
QY	2266	TAGGTTGCACTCTGTCAGGAGTCATCATCCCGAGGTGACAGTCTCTGAT	2312	Db	3273	CTGCCAAATATACCAACACTTGTGTTGAAATTTAAAGAAAAAAAGA	3322
Db	2253	TAGGTTGCACTCTGTCAGGAGTCATCATCCCGAGGTGACAGTCTCTGAT	2335	RESULT 5			
QY	2326	TCACAGCCTGTCAGCTTCTGTGTCAGTATTGGGTTCACAGAGTATGACTCTGAT	2312	AAFP8774			
QY	2313	TCACAGCCTGTCAGCTTCTGTGTCAGTATTGGGTTCACAGAGTATGACTCTGAT	2445	ID	AAFP89774	standard; DNA: 2733 BP.	
QY	2386	GGAACTCACTCCCACTGTAACCTTGAGGATACCGGAGGTGTC	2432	XX	AAFP89774		
Db	2373	GGAACTCACTCCCACTGTAACCTTGAGGATACCGGAGGTGTC	2505	XX	AAFP89774;		
QY	2446	TCTCTTATAGGTCAAAGATGTGACCTCTGGAGATGTCCTCCAGAACGTC	2492	AC			
Db	2433	TCTCTTATAGGTCAAAGATGTGACCTCTGGAGATGTCCTCCAGAACGTC	2565	XX			
QY	2506	CGCTCTGGCTGCACTGAAACTGTCCTCCCTGGAGATGTCCTCCAGAACGTC	2552	DE			
Db	2493	CGCTCTGGCTGCACTGAAACTGTCCTCCCTGGAGATGTCCTCCAGAACGTC	2525	XX			
Db	2566	TGAGTGGACCTGTGAGGGCTGCAACTTCACCTCTCTGTCGAGGAGGCTG	2612	KW			
QY	2553	TCAGATGGGACCTGTGAGGGCTGCAACTTCACCTCTGTCGAGGAGGCTG	2685	XX			
Db	2626	CGCTCTGGCTGCACTGAAACTGTCCTCCCTGGAGATGTCCTCCAGAACGTC	2672	OS			
QY	2746	CAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2792	XX			
Db	2613	CCCTCTGGCTGCACTGAAACTGTCCTCCCTGGAGATGTCCTCCAGAACGTC	2745	FH			
QY	2686	AAGACTACTTACGGTGGGAGAACCCAGCTGTCACCTCTGTCGAGGAGGCTG	2732	FT			
Db	2673	AAGACTACTTACGGTGGGAGAACCCAGCTGTCACCTCTGTCGAGGAGGCTG	2805	XX			
QY	2793	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2925	PN	W0200131003-A1.		
QY	2866	CTAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2952	XX	03-MAY-2001.		
Db	2733	CAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2865	XX	30-OCT-2000; 2000MO-FR03032.		
QY	2806	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2852	XX	99FR-0013629.		
Db	2793	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2925	XX	29-OCT-1999;		
QY	2866	CTAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2952	PR			
Db	2733	CAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2865	XX			
QY	2793	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2925	PA	(FABR) FABRE MEDICAMENT SA PIERRE.		
Db	2793	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2925	XX	XX		
QY	2866	CTAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2952	PT	New nucleic acid, expressed in tumours and lymphoid tissue is useful for		
Db	2733	CAGAGTACCATCTGCAAAACCATGATGTTCTGTGAAAGTGTGGCTG	2865	XX	Identifying agents for treating tumours and autoimmune disease		
QY	2793	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2925	XX	Claim 2; Page 56-60; 85pp; French.		
Db	2793	ACCTGACTGCACTCTGTCACCTGTCACCTGTCACCTGTCACCTGCA	2925	XX	The present sequence encodes a human protein expressed in tumour cells.		

cloning isolated cDNA; used for screening cDNA/genomic DNA banks and encodes a human protein, where the mutant forms of the gene that abnormal gene expression, or mutations are associated with particularly for diagnosis; or promoters and regulators of the gene, protein; as probes and primers for recombinant expression of the gene, as antisense therapeutic agents. The tumour expressed protein is useful, bind to it or interact with it. These agents that modulate its activity, specific antibodies and to screen agents that modulate its useful for treatment or prevention of it. These agents are potentially expression/activity of the protein, particularly associated with abnormal (autoimmune diseases and cancer) or viral, bacterial, fungal or parasitic infections.

		XX	Key	Location/qualifiers
Db	1861	TGCCCCCTAACACAAATTCTGAAAGCCCCAACAGCTTATGGGTCCAGGCGCTGTGCC	1920	FH
Qy	1978	TGCGTCCAGGACCAGAACACAGATCCACTCTCGTGTACAGATGTCACCTC	2037	FT
Db	1921	TGTGTCAGGACCAGAACAGATCCACTCTCGTGTACAGATGTCACCTC	1980	FT
Qy	2038	TCAAGCAACATCACAACAGACTTCACACTTCTCCCTTGGCAACACCGTC	2097	PN
Db	1981	TCACGCCAACACTCCAAACAGAGACTTCACACTTCTCCCTTGGCAACACCGTC	2040	XX
Qy	2098	ACTCTGCGAGGAGGCCAGCTCACCTCCAAAGGTGAAATCTCCATCACTTAC	2157	PR
Db	2041	ACTCTGCTGAGGGCCAAAGCTTCACTTCAACTTCAACTTCAACTTCAACTTCA	2100	XX
Qy	2158	CTCACTCTGTTGAGAACAGGGTAGGAAATCTCTGTCACCGACAGATGACTGAC	2217	PD
Db	2161	CTCGGATTCCTGAGGTGACTCAGGTCTCCAAATCTACAGCTGACGCTG	2337	XX
Qy	2276	GCAGTCATCATCCCGAGAGGTGACAGGGTACAGGGTACAGGGGTTCTCACAGCC	2277	PR
Db	2221	GCAGTCATCATCCCGAGAGGTGACAGGGTACAGGGTACAGGGTACAGGTG	2220	XX
Qy	2338	AGCCTGCGATGACTGACTTATGGGTACAAACAGATATGCTCGATGGAACTC	2397	PA (FABR) FABRE MEDICAMENT SA PIERRE.
Db	2341	CGAGCTGACTTTCACCTCTGGATCTGGGTACAGATATGACTCTGAGAACCC	2340	XX
Qy	2458	TCAAATGTTGACCCAGTCTGAGTTGGGAGATCAACACCATCCCGTCAGTC	2457	PT Delneste Y, Magistrelli G, Jeannin P, Bonnefoy J;
Db	2461	AGCTGCTGATGACTGACTTTCACCTGGAGATCTGGAGATCCACCGTCAGTC	2460	XX
Qy	2518	AGTCACAGAACACTGACCTCTGGAGATCTGGAGATCCACCGTCAGTC	2577	DR WPI: 2001-328651-34.
Db	2401	TCCATGATGTCGACCTCTGGAGATCAACACCATCCCGTCAGTC	2520	DR-PSDB; AAB83651.
Qy	2578	TGTGATGCTGCACTTCACCTCTGGAGATCTGGAGATCCACCGTCAGTC	2637	PS
Db	2521	TGTGATGCTGCACTTCACCTCTGGAGATCTGGAGATCCACCGTCAGTC	2697	XX
Qy	2638	GTGGCTGACTACCATGTCATGTCAGCAGCTGTGCTGGATCAGAGACTTAC	2640	CC
Db	2581	GTGGCTGACTACCATGTCATGTCAGCAGCTGTGCTGGATCAGAGACTTAC	2757	CC
Qy	2698	GTGGCTGAGAACCCAGCTATGCTCTCCCTGAGAGAGTCACC	2700	CC
Db	2641	GTGGCTGAGAACCCAGCTATGCTCTCCCTGAGAGAGTCACC	2790	CC
Qy	2758	ATCGCCAAACCTAGTTCTGGCTGAAGTG	2793	CC
Db	2701	ATCGCCAAACCATAGATTCTGGCTGAAGTG	2733	CC
RESULT	6			XX
ARF89775		Query Match		Location/qualifiers
ID	ARF89775	Sequence 2610 BP; 634 A; 744 C; 644 G; 588 T; 0 other;	1..2610	1..2610
XX		Score 2603.6; DB 22; Length 2610;		/*tag= a
AC	ARF89775;	Best Local Similarity 78.1%; Score 2603.6; DB 22; Length 2610;		/product= "tumour expressed protein"
XX		Matches 2606; Conservativeness 99.8%; Preid. No. 0; Mismatches 4; Indels 0; Gaps 0;		
DT	23-JUL-2001 (first entry)	Query 181 ACGGGACGGAGCTTACGGCTGCAAAAGACTCTGAGTACCATATGAGTACAGGGGTG	240	
XX		DB 1 ACGGGACGGAGCTTACGGCTGCAAAAGACTCTGAGTACCATATGAGTACAGGGGTG	300	
DE	Nucleotide sequence of a human protein expressed in tumour cells.	Qy 241 GACACCCACGGGTCACGTTGGGGGCGCTGGGATACCCGGGCTGACCCAGC	120	
XX		DB 61 GACACCCACGGGTCACGTTGGGGGCGCTGGGATACCCGGGCTGACCCAGC	360	
DE	Tumour cell; immunological disease; autoimmune disease; cancer; infection; ss.	Qy 301 CTGGCTGACCCGGTCAAGGACCGAGAAGGCTCTCTCTCTGCAACGGGGGACTTC	180	
XX		DB 121 CTGGCTGACCCGGTCAAGGACCGAGAAGGCTCTCTCTCTGCAACGGGGGACTTC	420	
OS	Homo sapiens.	Qy 361 GATATGAGGAGGACGACTGATGAGCTTGGCTGAGGCGCTACTCCCTGGCAACAGC	240	
		DB 181 GATATGAGGAGGACGACTGATGAGCTTGGCTGAGGCGCTACTCCCTGGCAACAGC	480	
		Qy 421 ATTCGGTTGAGGAGTGGATGAGCTTGGCTGAGGCGCTACTCCCTGGCAACAGC	300	
		DB 241 ATTCGGTTGAGGAGTGGATGAGCTTGGCTGAGGCGCTACTCCCTGGCAACAGC	540	
		Qy 481 GAGCTGGATGACAGTGTCTGAGTCACTGGGGACTGTACTCTGCAACTGGT	360	
		DB 301 GAGCTGGATGACAGTGTCTGAGTCACTGGGGACTGTACTCTGCAACTGGT	600	
		Qy 541 CGGGCGACTACATGGCTCACACGGACATGGCTACGGCAACCCACACTGATG		

QY	2761	TGCGAAACCATAGATTCTGGCAGAACGTG	2790	Db	194	CTCTTGCCACCCAGTGTGACCCGTGACAATTA	TACTCGAGAGAAGGTCTTCTCTGTAACG	253		
Db	2581	TGCAAACCATAGATTCTGGCAGAACGTG	2610	QY	1034	TCCGCCAGCTTCGACAGACAAAGATTATTC	TACACACACACGCCCTGGATCCAAAG	1093		
XX				Db	254	TGCGCCACAGTGCACAGACAAAGATTATTC	TACACACACGCCCTGGATCCAAAG	313		
AC				QY	1154	GGCAGCTGAGCTGCCCTGGTGAAGACCC	ACTGCCAACCTGCAACCCAGGT	1213		
XX				Db	374	GGCAGIGAGCTGCCCTGGTGAAGACCC	ACTGCCAACCTGCAACCCAGGT	433		
DT	08-MAY-2001	(first entry)		QY	1214	TCTTCAAACCAACAAACAGACCTGACGCC	ATATGGTTCCTACTCCATAGGT	1273		
XX				Db	314	GAGAGACACTCATGTA	AAATGGCCAAATGTGAGGACCTTGAG	373		
DE		Human TR13 receptor coding sequence SEQ ID NO: 1.		QY	1274	CAGACTGTACCGCTGCCCTGAGGACTG	ACCTGACCTGCCATATGGTTCCTACTCCATAGGT	493		
XX				Db	494	CAGACTGTACCGCTGCCCTGAGGACTG	ACCTGACCTGCCATATGGTTCCTACTCCATAGGT	553		
KW		Human; tumour necrosis factor receptor; TR13; TR4; infection; cancer; autoimmune disease; allergy; inflammatory disease; graft rejection; apoptosis; cardiovascular disease; aneurysm; ds.		QY	1334	GGACAGCGGCCACAAACATGAAACGACCG	GTCTCAGGGGACAACATGAGTACATAGT	1393		
OS				Db	554	GGACACGGCTGCCACAAACATGAAACGACCG	GTCTCAGGGGACAACATGAGTACATAGT	613		
XX				QY	1394	AGSGCATGACAGGCTGGAGGTGCGT	GGTGTACACAGCTGCCGGCTCAG	1453		
PR	14-JUL-2000;	2000WO-US19343.		Db	614	AGGCACTGACAGGCTGGAGGTGCGT	GGTGTACACAGCTGCCGGCTCAG	673		
XX				QY	1454	ACATAGACTCATGATCTCACTCTGGT	GTGCCAGATTAGACCTCCGAGTGTGA	1513		
PR	16-JUL-1999;	99US-0144087.		Db	674	ACATAGACTCATGATCTCACTCTGGT	GTGCCAGATTAGACCTCCGAGTGTGA	733		
PR	18-AUG-1999;	99US-01449450.		QY	1514	TGCGAGACAGAGAAAGAGGTG	GGCCAGATCATGATCTCACTCTGGT	1573		
PR	20-AUG-1999;	99US-0149112.		Db	734	TGCGAGACAGAGAAAGAGGTG	GGCCAGATCATGATCTCACTCTGGT	793		
XX	10-SEP-1999;	99US-0153089.		QY	1574	CTGTAACGCTGAGCTCTACTCATG	GGTGTGAGCTCCGAGCTCTTG	1633		
PA				Db	794	CTGTAACGCTGAGCTCTACTCATG	GGTGTGAGCTCCGAGCTCTTG	853		
(HUMA)		HUMAN GENOME SCI INC.		QY	1634	AGAGTGGAAAGGTTCAAGGAACAA	CGACCTTACCTACATGATCTG	1693		
PA				Db	854	AGACCTGGAAAGGTTCAAGGAACAA	CGACCTTACCTACATGATCTG	913		
PR				QY	1694	CCAGAGCTTCACCTGGCCTTCAGAG	GGGACCAACTTTCATGAGCAAGGAGT	1753		
PT				Db	914	CCAGAGCTTCACCTGGCCTTCAGAG	GGGACCAACTTTCATGAGCAAGGAGT	973		
XX				QY	1754	CCATGACCTTGCACAGACTTACCCAT	ATGTCACCATGTCACCATGTCAC	1813		
PS				Db	974	CCATGACCTTGCACAGACTTACCCAT	ATGTCACCATGTCAC	1033		
CC		Claim 2; Page 366-369; 418pp; English.		QY	1814	CTACTGCCTCCCTGGCTTAGAGCT	TCTGTCCTCCCTGGCTCCTCCGACCTCTG	1873		
CC				Db	1034	CTACTGCCTCCCTGGCTTAGAGCT	TCTGTCCTCCCTGGCTCCTCCGACCTCTG	1093		
CC		The present invention provides the protein and coding sequences of the human tumour necrosis factor receptors TR13 and TR4. These sequences are useful in the diagnosis and treatment of many diseases, including cancer, autoimmune diseases, cardiovascular disorders, allergies, neurodegenerative diseases, graft rejection, inflammation, aneurysms and infections.		QY	1874	CTGCTGTTACTATATTGAGG	ATGAGCTTGTGAGGACTCTG	1933		
XX				Db	1094	CTGCTGTTACTATATTGAGG	ATGAGCTTGTGAGGACTCTG	1153		
SQ	Sequence 2554 BP;	642 A; 722 C; 588 G; 602 T; 0 other;		QY	1934	TCTCTAAAGCCACCCGCTTATGGT	TGAGGCTGTGAGGACCA	1993		
Query Match	75.8%	Score 2527.4;	DB 22;	Length 2554;	Db	1154	TCTCTAAAGCCACCCGCTTATGGT	TGAGGCTGTGAGGACCA	1213	
Best Local Similarity	99.9%	Pred. No. 0;	Mismatches 0;	Indels 1;	QY	1994	AGACACAGATCACTCTG	GGGACCTCTG	2053	
Matches	2559;	Conservative		Gaps 1;	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
QY	794	CCAGAGCTTCACCTGGCCTTCAGT	AGGACAACTTACCCAAAGCTGT	CTGGAGAACATG	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
Db	15	CGCGAGCCTTCAGTATGGACAA	AGTACCTTCATGAA	AGTACATGCCA	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
QY	854	TACAGGGTGTGCTTA	ACTCTGAGCTTCCCTG	CAACCTGAGCT	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
Db	75	TACAGGGTGTGCTTA	ACTCTGAGCTTCCCTG	CAACCTGAGCT	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
QY	914	AGCAGGCTTCCTCTG	CAACTCTGAGCTTCCCTG	CAACCTGAGCT	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
Db	135	AGCAGGCTTCCTCTG	CAACTCTGAGCTTCCCTG	CAACCTGAGCT	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273	
QY	974	CTCTCTGACACACTG	TGAGCTGACAA	TATCTGAGAGAAGGAT	CTCTCTG	Db	1214	AGAACACAGATCCACTCTG	GGGACCTCTG	1273

QY	3314	AATTAACCAACCTCTCTGCTGCTCAACCTGCCRATATAACCCACACTGTTGTA	3313
Db	2474	ACCCAAACCTCTCTGCTGCTCAACCTGCCRATATAACCCACACTGTTGTA	3313
Db	2474	ACCCAAACCTCTCTGCTGCTCAACCTGCCRATATAACCCACACTGTTGTA	2533
QY	3314	AATTAACCAACCTCTCTGCTGCTCAACCTGCCRATATAACCCACACTGTTGTA	3313
Db	2534	AATTAACCAACCTCTCTGCTGCTCAACCTGCCRATATAACCCACACTGTTGTA	2534
RESULT 8			
ID	AA241991	AA241991 standard; cDNA; 1717 BP.	
XX	XX	31-JAN-2000 (first entry)	
AC	AC	XX	
DE	DE	Human endometrium tumour cDNA derived EST 11.	
XX	XX	Endometrium; human; tumour; cancer; anticancer; cytosstatic; EST: treatment; uterine; gene therapy; expressed sequence tag; ss.	
KW	KW	OS	
XX	XX	Homo sapiens.	
OS	OS	PN	
XX	XX	DE19817948-A1.	
PD	PD	XX	
XX	XX	21-OCT-1999.	
PF	PF	XX	
XX	XX	98DE-1017948.	
PR	PR	XX	
XX	XX	17-APR-1998; 98DE-1017948.	
PA	PA	XX	
XX	XX	(META-) METAGEN GES GENOMFORSCHUNG MBH.	
PT	PT	XX	
XX	XX	Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;	
DR	DR	XX	
WPI; 1999-591957/51.	P-PSDB; AAY59971, AAY59972, AAY59973.	XX	
PT	PT	XX	
XX	XX	New nucleic acid sequences expressed in uterine cancer tissues and derived polypeptides for treatment of uterine and endometrial cancer and identification of therapeutic agents -	
PS	PS	XX	
XX	XX	Claim 3; Page 172; 444pp; German.	
This invention describes novel human nucleic acid (cDNA) sequences (A), that are highly expressed in uterine tumour tissue and which have anticancer and cytostatic activity. (A) are used (i) for recombinant expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTS (expressed sequence tags) from a particular tissue type before comparison of expression patterns. This allows a significantly longer fragment of the gene to be revealed, so should reduce the number of failures associated with the fact that ESTs from different libraries may represent different parts of the same unknown gene, distorting the estimated frequency of occurrence in a particular tissue. AA241981-242121 represent EST fragments derived from a human endometrium tumour cDNA library which encode the protein sequences represented in AAY59941-Y60328.			
SQ	SQ	Sequence 1717 BP; 416 A; 492 C; 388 G; 421 T; 0 other;	
Query Match 51.1%; Score 1705; DB 20; Length 1717;			
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indices 1; Gaps 1;			
Matches 1716; Conservative 0; Mismatches 0; Indices 1; Gaps 1;			
1610 ATTCTAGGACCAACACTCTCTGAGACGTG3GAAAGGTCTCAAAGCAACAGTCTATA 1669			

Db	1	ATTCCTAGGACCAACACTCCCTGGAGACGGAGAAAGGTTCAAAAGGCAACAGSPCTATA	Db	1081	CTACTTAGCTGTGGAGACCCAAAGCTATGCTCTGGGATTCTCTCTGAGCAGA
Oy	1670	CCTACATCATGAGGAGAACACTAACCGAGCTCACCTGGGTTCCAGAGGACACTT	Qy	2750	GACTCACCATCTGCACAAACAGAAGATATCTGCTGAAGGGCATCTCAGGACACT
Db	61	CCTACATCATGAGGAGAACACTAACCGAGCTCACCTGGGTTCCAGAGGACACTT	Db	1141	GACTCACCATCTGCACAAACAGAAGATATCTGCTGAAGGGCATCTCAGGACACT
Oy	1730	TCATGAGGAGAACACTAACCGAGCTCACCTGGGTTCCAGAGGACACTT	Qy	2810	GTAATGCCATCCCTGCTCACCGCTTACGGCTACTTGGGAAAGGAAAGAATCAAACATG
Db	121	TCATGAGGAGAACACTAACCGAGCTCACCTGGGTTCCAGAGGACACTT	Db	1201	GTACTGCACATCCGCTCACCGCTTACGGCTACTTGGGAAAGGAAAGAATCAAACATG
Oy	1790	CCATGATCATGAGGAGAACACTAACCGAGCTCACCTGGGTTCCAGAGGACACTT	Qy	2870	AGTACAAGTACTCAAGCTGGTATGATGCTACTCTCAAGGACTGTGAGCCCTGAG
Db	241	TCGGCTCTCCGACCTCTGCTCTGCTGTACTATATTGACCGAGATTCAGGACCT	Db	1261	AGTACAAGTACTCCAAAGCTGGTATGATGCTACTCTCAAGGACTGTGAGCC
Oy	1910	GCCACTCTGCTGCCCTTAACAAATCTGGAAGGCCACCGCTPATGTTGAGGACCT	Qy	2930	CTGACAGTGGCCATCATGGAAAGGCCACCGCTTACGGCTACTTGGAAAAGAATCAAACATG
Db	301	GCACTCTGCTGCCCTTAACAAATCTGGAAGGCCACCGCTTACGGCTACTTGGAGGCT	Db	1321	CTGACAGTGGCCATCATGGAAAGGCCACCGCTTACGGCTACTTGGAGGACCT
Oy	1970	GTGCGCTGGCTCAGGAGAACACAGACAGACAGACAGACAGACAGACAGACAGAC	Qy	2990	AGAA-TCACTCTGGGAGATAAATCTACCTCAAGGAGCTCCATCTGAGGTTG
Db	361	GTGTCGCTGAGTCAGGAGAACACAGACAGACAGACAGACAGACAGACAGAC	Db	1381	AGAA-TCACTCTGGGAGATAAATCTACCTCAAGGAGCTCCATCTGAGGTTG
Oy	2030	GCACTCTCAGGAAACACTCCACAGGACTTCAACTACAGACTCTCGCTTGGCTACATGATT	Qy	3049	ACTCAGTGGCGCTGAGAGACATCTCAGGAGCCAGACATGGACCTGTGAGGAGCTG
Db	421	GCACTCTCAGGAAACACTCCACAGGACTTCAACTACAGACTCTCGCTTGGCA	Db	1441	ACTCAGTGGCGCTGAGAGACATCTCAGGAGCCAGACATGGACCTGTGAGGAGCTG
Oy	2090	ACACCGTCACTCTGCTGGAGGCCAGCTTCAACTTCAAAAGGGTTGAATATCTCATC	Qy	3169	CCACCATCTGCAACCCACTCTGGGATCATCTCTGGGCCATCTGAGATGTTG
Db	481	ACACCGTCACTCTGCTGGAGGCCAGCTTCAACTTCAAAAGGGTTGAATATCTCATC	Db	1561	CCACATCCGCAACCCACTCTGGGATCATCTCTGGGCCATCTGAGATGTTG
Oy	2150	ACTTACCTCTGCTCTGGAACAGGTTAGGAATAGCTCTGTCACCGACATCTCCATC	Qy	3229	AATTCAGTCCTTTTATAGTACCTCCAAACCTCTTCCTGCTGCTGCTCAAACCTG
Db	541	ACTTACCTCTGCTCTGGAACAGGTTAGGAATAGCTCTGTCACCGACATCTCCATC	Db	1621	AATTCAGTCCTTTTATAGTACCTCCAAACCTCTTCCTGCTGCTGCTCAAACCTG
Oy	2210	TCATGACTCTGGATTCCTGGAGGTTAGGAATAGCTCTGTCACCGACATCTCCATC	Qy	3289	CAATATACCCACACTTGTGTAATTAAAAAA
Db	601	TCATGACTCTGGATTCCTGGAGGTTAGGAATAGCTCTGTCACCGACATCTCCATC	Db	1681	CAATATACCCACACTTGTGTAATTAAAAAA
Oy	2270	TCTGCCAGGACATCATGCCAGAGGAGACAGGGCTACAGGGGGTTCTCAC	RESULT 9		
Db	661	TCTGCCAGGACATCATGCCAGAGGAGACAGGGCTACAGGGGGTTCTCAC	ID	ABV23150	
Oy	2330	ACGCTGTCAGCTTGTGCTGATCCACTTATGGGTGACACAGATATGACTCTGGATGAA	XX	ABV23150	
Db	721	ACGCTGTCAGCTTGTGCTGATCCACTTATGGGTGACACAGATATGACTCTGGATGAA	AC	ABV23150;	
Oy	2390	TCACCTCCCACGCTGACTTCCACCTGGAGCTTGGGATAACCGAGCTGATCT	XX	16 - SEP - 2002	(first entry)
Db	781	TCACCTCCCACGCTGACTTCCACCTGGAGCTTGGGATAACCGAGCTGATCT	XX	Human prostate expression marker cDNA	23141.
Oy	2450	TCTAGGTGAGTCACAGAAACTCTGCTCTGGAGAGTGTGCTGCTGCCAGGAACGTGTCAG	XX	KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; pharmacogenomic marker; gene; ss.
Db	841	TCTAGGTGAGTCACAGAAACTCTGCTCTGGAGAGTGTGCTGCTGCCAGGAACGTGTCAG	XX	OS	Homo sapiens.
Oy	2510	TCTAGGTGAGTCACAGAAACTCTGCTCTGGAGAGTGTGCTGCTGCCAGGAACGTGTCAG	XX	PN	WO200160860-A2.
Db	901	TCTAGGTGAGTCACAGAAACTCTGCTCTGGAGAGTGTGCTGCTGCCAGGAACGTGTCAG	XX	PD	23 - AUG - 2001.
Oy	2570	ATGGGACTCTGCTGACTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	XX	PP	20 - FEB - 2001; 2001WO-US05171.
Db	961	ATGGGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	XX	PR	17 - FEB - 2000; 2000US-183319P.
Oy	2630	TCTGCTCAGTGTGCTGACTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	PR	16 - MAR - 2000; 2000US-189862P.	
Db	1021	TCTGCTCAGTGTGCTGACTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	PR	25 - MAY - 2000; 2000US-20754P.	
Oy	2690	CTACTTACCTGCTGGAGAACCAAGCTATGCTGGGAAATTCTCTGCTGAGAGA	PR	18 - JUN - 2000; 2000US-211314P.	
Db			PR	13 - DEC - 2000; 2000US-25581P.	
Oy			PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
			XX		

XX	PI	schlegel R, Endege WO, Monahan JE;
XX	WPI:	2001-662795/76.
DR	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer	DR
PT	The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:	PT
PT	(a) assessing whether a patient is afflicted with prostate cancer;	PT
CC	(b) monitoring the progression of prostate cancer in a patient;	CC
CC	(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;	CC
CC	(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;	CC
CC	(e) selecting a composition for inhibiting prostate cancer in a patient;	CC
CC	(f) assessing the prostate cell carcinogenic potential of a compound;	CC
CC	(g) determining whether prostate cancer has metastasized in a patient;	CC
CC	(h) assessing the aggressiveness or indolence of prostate cancer in a patient;	CC
XX	(I) is also useful as a pharmacodynamic or pharmacogenomic marker.	XX
SQ	Sequence 1299 BP; 321 A; 373 C; 308 G; 294 T; 3 other;	QY
Query Match	35.2%; Score 1172.8; DB 23; Length 1299;	QY
Best Local Similarity	99.8%; Pred. No. 0; Mismatches 1174; Conservative 0; Indels 0; Gaps 0;	Db
Matches	1174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	Db
QY	1145 ACCTTGAGGGCCAGTGAAGCTGCGCTCTGGTGTGAAGACCCACTGCCACCTGCA 1204	QY
Db	3 ACCTGAGGGCCAGTGAAGCTGCGCTCTGGTGTGAAGACCCACTGCCACCTGCA 62	Db
QY	1205 ACCCAGGCTCTCAAAACACACAGCAGCCTGCAACAGCTTACAGCTTACATGGTCTACT 1264	QY
Db	63 ACCCAGGCTCTCAAAACACACAGCAGCCTGCAACAGCTTACAGCTTACATGGTCTACT 122	Db
QY	1265 CCAATGCTCAGACTGTACCCGCTGCCCTCGAGGACTGAACTCTGTTGGATTGAAAT 1324	QY
Db	123 CCAATGCTCAGACTGTACCCGCTGCCCTCGAGGACTGAACTCTGTTGGATTGAAAT 182	Db
QY	1325 ACAATGCTGAAACAGCTGCCACAACTATGAAACAGCAGCTCTCAGCTGGATCACT 1384	QY
Db	183 ACAATGCTGAAACAGCTGCCACAACTATGAAACAGCAGCTCTCAGCTGGATCACT 242	Db
QY	1385 TCGAGTACAGGGCATGACGGCTGGAGGTGGTGTGATCAATTACACAGCTGCT 1444	QY
Db	243 TCGAGTACAGGGCATGACGGCTGGAGGTGGTGTGATCAATTACACAGCTGCT 302	Db
QY	1445 GAGCCCTCAGAATGACTTATGATCTACTCTCTGGTGTGCAATTAGACCTCCCG 1504	QY
Db	303 GAGCCCTCAGAATGACTTATGATCTACTCTGGTGTGCAATTAGACCTCCCG 362	Db
QY	1505 AGTCGGTGTGGCAGACAGAGATAAAGGGTGGCCAGAACTCACATTGTCCTTGAGA 1564	QY
Db	363 AGTCGGTGTGGCAGACAGAGATAAAGGGTGGCCAGAACTCACATTGTCCTTGAGA 422	Db
QY	1565 CCCTCTGTTCTGTGACTGTGACTCTACTCTCATGGGGTGTGAACTCTAGGACCAACA 1624	QY
Db	423 CCCTCTGTTCTGTGACTGTGACTCTACTCTCATGGGGTGTGAACTCTAGGACCAACA 482	Db
QY	1625 CTCCCTGGAGACGCTGGAAAGGTCCAAAGGACAAAGCAGTGTGAACTCTAGG 1684	QY
Db	483 CTCCCTGGAGACGCTGGAAAGGTCCAAAGGACAAAGCAGTGTGAACTCTAGG 542	Db
QY	1685 AGAACACTACACGAGCTTACCCGGCTTCCAGAGGACACTTTCATGGCAAGCA 1744	QY
Db	543 AGAACACTACACGAGCTTACCCGGCTTCCAGAGGACACTTTCATGGCAAGCA 602	Db
QY	1745 GGAATACACAAATGAGCTGTCAGATCTACTCCATGATGTCACCACTATGTTATGATG 1804	QY
RESULT 10		QY
ID	ABV28991	QY
ID	ABV28991 standard; cDNA: 1299 BP.	QY
XX		QY
AC	ABV28991;	QY
XX		QY
DT	16-SEP-2002 (first entry)	QY
XX		QY
DE	Human prostate expression marker cDNA 28992.	QY
XX		QY
KW	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; gene; ss.	QY
XX		QY
OS	Homo sapiens.	QY
XX		QY
PN	WO2001060860-A2..	QY
XX		QY
PD	23-AUG-2001.	QY
XX		QY
PF	20-FEB-2001; 2001WO-US050171.	QY
XX		QY
PR	17-FEB-2000; 2000US183319P.	QY
PR	16-MAR-2000; 2000US199862P.	QY
PR	15-MAY-2000; 2000US207454P.	QY
PR	09-JUN-2000; 2000US211314P.	QY
PR	18-JUL-2000; 2000US219007P.	QY
PR	13-DEC-2000; 2000US225281P.	QY
XX		QY
PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	QY
XX		QY
PT	Schlegel R, Endege WO, Monahan JE;	QY
XX		QY
DR	WPI: 2001-662795/76.	QY

XX
 XX Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer
 XX
 PS Claim 1; Page 6131; 11750pp; English.

XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV0010 ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC
 (a) assessing whether a patient is afflicted with prostate cancer;
 CC
 (b) monitoring the progression of prostate cancer in a patient;
 CC
 (c) assessing the efficacy of a test compound to inhibit prostate
 cancer in a patient;
 CC
 (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 in a patient;
 CC
 (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC
 (f) assessing the prostate cell carcinogenic potential of a compound;
 CC
 (g) determining whether prostate cancer has metastasized in a patient;
 CC
 (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC
 (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 Sequence 1299 BP; 321 A; 373 C; 308 G; 294 T; 3 other;

Query Match Similarity 35.2%; Score 1172.8; DB 23; Length 1299;
 Best Local Similarity 99.8%; Pred. No. 0; Matches 1174; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1145 ACTTGTAGGGGCACTGAACTCTGCTGCGCTGGTGTGAAGACCCACTGCCACCCCTCA 1204
 Db 3 ACTTGAGGGGCACTGAACTCTGCTGCGCTGGTGTGAAGACCCACTGCCACCCCTCA 62

QY 1205 ACCCAGGTCTCTCAARACCAACACAGACCTGCCAGCCTGCCATAGTTCTACT 1264
 Db 63 ACCCAGGTCTCTCAAAACCAACAGACCTGCCAGCCTGCCATAGTTCTACT 122

QY 1265 CCAATGGCTCAGACTGACCGCTGCCCTGCCAGGACTGACCTGCTGGGATTGAT 1324
 Db 123 CCAATGGCTCAGACTGACCGCTGCCCTGCCAGGACTGACCTGCTGGGATTGAT 182

QY 1325 ACAATGGTGCAGACAGCTGCCACAAACATGGAAACGACCGTCTCACTGGATCACT 1384
 Db 183 ACAAAATGGTGCAGACAGCTGCCACAAACATGGAAACGACCGTCTCACTGGATCACT 242

QY 1385 TCGAGTACAAGGCATGACAGGTGGAGGTGGCTGACGCTGCTGAGTCACT 1444
 Db 243 TCGAGTACAAGGCATGACAGGTGGAGGTGGCTGACGCTGCTGAGTCACT 302

QY 1445 GAGCCCTCAGACATGACTGATGATCTCACTCTGGTGTGCCAGGATTGACCTCCGC 1504
 Db 303 GAGCCCTCAGACATGACTGATGATCTCACTCTGGTGTGCCAGGATTGACCTCCGC 352

QY 1505 ACTGGGTGATGGCAGACAGAGAAATAGGTTGGCCAGAAATACATTTGCTTGAGA 1564
 Db 363 ACTGGGTGATGGCAGACAGAGAAATAGGTTGGCCAGAAATACATTTGCTTGAGA 422

QY 1565 CCTCTCTGTCGTCGTCGACTGCTACTCTATGGGGTGATGATGAGGCAACA 1624
 Db 423 CCTCTCTGTCGTCGACTGCTACTCTATGGGGTGATGAGGCAACA 482

QY 1625 CCTCTCTGAGGAGCTGGAAAGGTTCAAAGCCAAACAGTCTATACATCATGGAG 1684
 Db 483 CCTCTCTGAGGAGCTGGAAAGGTTCAAAGCCAAACAGTCTATACATCATGGAG 542

QY 1685 AGACACTACACAGAGCTTACCTGGGCTTCAGAGGACCACTTCATGAGGAAAGA 1744
 Db 543 AGACACTACACAGAGCTTACCTGGGCTTCAGAGGAAAGA 602

QY 1745 GAGAGTACACCATGAGGTTGCAAGATCTACCTCCATGTCACAAATGTTAGATG 1804
 Db 603 GAGAGTACACCATGAGGTTGCAAGATCTACCTCCATGTCACAAATGTTAGATG 662

QY 1805 GGGGGCCTTAATGCGCCTGTGCCCTAGAGCTCTGATGGGCTCCCTGCA 1864
 Db 663 GGTGSGCTTACTGCGCTGCGCTAGAGCTCTGATGGGCTCCCTGCA 722
 QY 1865 CTCCTGCTCTGTTACATATGACCGAGATCAGGACCTGCCACTCCCTGGCC 1924
 Db 723 CCTCTGCTCTGTTACATATGACCGAGATCAGGACCTGCCACTCCCTGGCC 782

QY 1925 CTAACAAATCTGAAAGCCACCACTATGTTGGTGTCCAGGCCCTGGTGTGGTC 1984
 Db 783 CTRACACAAATCTGAAAGCCACCACTGGTGTGGTGTGGTC 842

QY 1985 CAGGGACCAAGACAAAGATCCACTCTGCTGCTACATGATGATGACCTTCACGCA 2044
 Db 843 CAGGGACCAAGACAAAGATCCACTCTGCTGCTACATGATGACCTTCACGCA 902

QY 2045 ACACCTCCACCAAGGACTTCAACTACACTACACTCTCCGTTGGCAACACGGTACTCTG 2104
 Db 903 ACACCTCCACCAAGGACTTCAACTACACTCTCCGTTGGCAACACGGTACTCTG 962

QY 2105 CTGGAGGCCAACGACTCTCACTACACTCTCCGTTGGCAACACGGTACTCTG 2164
 Db 963 CTGGAGGCCAACGACTCTCACTACACTCTCCGTTGGCAACACGGTACTCTG 1022

QY 2165 TCTGTGAAACCAAGGGTAGGAAATGCTGTGTCACGCCATGTCACCTGCCGA 2224
 Db 1023 TCTGTGAAACCAAGGGTAGGAAATGCTGTGTCACGCCATGTCACCTGCCGA 1082

QY 2225 TCTCTGAGGGTAGCTCAGGTCTCCAAATCTACACGGCTACGCTGCTGCCAGGAGTC 2284
 Db 1083 TCTCTGAGGGTAGCTCAGGTCTCCAAATCTACACGGCTACGCTGCTGCCAGGAGTC 1142

QY 2285 TCATCCCCCAGAGGTGACAGGCTACAGGGCTACAGGGGG 2320
 Db 1143 TCATCCCCCAGAGGTGACAGGCTACAGGGGG 1178

RESULT 11
 AAF8977
 ID AAF8977 standard; DNA; 1149 BP.
 XX
 AC AAF8977;
 XX
 DT 23-JUL-2001 (first entry)
 XX
 DE Nucleotide sequence of a human protein expressed in tumour cells.
 XX
 KW Tumour cell; immunological disease; autoimmune disease; cancer;
 KW infection; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 CDS
 FT 1..1149
 FT /*tag= a
 FT /product= "tumour expressed protein"
 XX
 PN WO20131003-A1.
 XX
 PD 03-MAY-2001.
 XX
 PR 30-OCT-2000; 2000WO-FR03032.
 XX
 PR 29-OCT-1999; 99FR-0013629.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PI Delheste Y, Magistrelli G, Jeannin P, Bonnefoy J;
 XX
 DR WPI; 2001-328651/34.
 DR P-PSDB; AAB83853.
 XX
 New nucleic acid, expressed in tumours and lymphoid tissue is useful for

Best local Similarity 60.5%; Pred. No. 8 2e-278; Matches 1755; Conservative 0; Mismatches 1118; Indels 28; Gaps 8;		Db	118B CAACCTGGATTTTATAACATGGATCCTCTTGGCATCCCTGTCCTCCGGAAACAT 1247
Qy	192 CGTTCAGGCCCTCAGCAAGAGTCTGAGTACCACTATGAGTACCGGCTGTCACACGGG 251	Qy	1263 CTCCCATGCCTC--AGACTGTACCCGCTGCCCCCTGCAAGGACTGAACTTCACCTGCGTGGGAT 1319
Db	171 GCTTCCCTCTTGCCAGGAGAAGATATCAGTTGATATAAGGGATAGTGG 230	Db	1248 TCAGATGGAAACAAAGATGTAGACCGCTGTCAGCAGGAAAGGAGCTGACTGGCT 1307
Qy	252 TTTCACTGGAGGGTGCCTGCCCCATACCCGGCTGTGACAGGCTGTCACACGGG 311	Qy	1320 TGAATACAATGGGGAACACGGTGGCCACAAACATGAAAGACGCCCTCAGTGGAT 1379
Db	231 CTCCAGGTGAGAGTGTGCTCCATTCACATTCAGCTGACTGCTGTCAGCAGGCTGACCC 290	Db	1308 TGAATATAATGGTGAATGTCCTCTGCAACATGAAACATTCCTGCTCAATGTTG 1367
Qy	312 CCTCAAGGGCACCGAGTGTCTCTCTGACACGGGGAGTTCTGATAGGA 371	Qy	1380 CAACTCGGTACAGGGCATGACAGGGGGGGTGGCTGTCAGCACATTACAGC 1439
Db	291 CCACTGAGGCAAAAGATGCACTTCTCCTGAGGAGCTATTCCTTGAGAGTCTAGAAATGAA 350	Db	1368 GAATCAAGTGGATGATGATGGTGGAGGTGCTGGAGATCATTCAGAGTG 1427
Qy	372 CCACTGAGGCAAAAGATGCACTTCTCCTGAGGAGCTATTCCTTGAGAGTCTAGAAATGAA 431	Qy	1440 TGCCTGGAGCTCAGACAATGACTTCATGATTCACACTCTGGTGTGCAAGGTTAGAC 1499
Db	351 CCAAGGATGCACTAAGTGTGGTGAAGGACCTATTCCTTGAGAGTCTAGAAATGAA 410	Db	1428 GCCTGGAGGTCTGACAGATGATTACCTGACTTAACCTGCAATCCAGGATTAAAC 1487
Qy	432 TCACTGGATGAGTCGCCATGGCTTCAGCACACATGGCTGGATGA 491	Qy	1500 TCCGAGTGGGATGGAGACAGAGATAAAGGGTGGCCAGACATCACATTGCT 1559
Db	411 TCAATGGATGATGTCGGCGAGGATTCTACATCGCACATTCATGACACTGTTG 470	Db	1488 ACCACATCTATGACTGGACAC--GGTTCTGAACTAGGAAATACTATGGCT 1544
Qy	492 CAGTGTGCTGAGTGTCCA--CGGGACTGACTCTGTCAGTGTGGTCCCAGGGGA 548	Qy	1560 TGAACCCCTCTGTCGACTGACCTGACCTCTACTCATGGTGGTGTGAC 1619
Db	471 GGCCCCCTGACAGCAGGGCAGGGCTAACACTCTCTGATGTCCTGGAA 530	Db	1545 TGAGACCCCTCTGTCGACTGTCGTTGACTTCATGGTGGATTAATAGAAAG 1604
Qy	549 CTACATCGCCCTCACACGGGAGATCACAGCCACACTGATGTCAGGGTCAACCTGA 608	Qy	1620 CAACACTCTGTGAGGCTGGAAAGGTTCCAAAGGAAACAGTCCTATACCTACAT 1679
Db	531 CTACATGAACTCTAATCTGTGATGACTCTGTCAGGGTCACTGTCAGCTAA 590	Db	1605 TACAATGTTGAGATCTGGGGTGGACCAAAGAAACAGCTACACCCATTCAT 1664
Qy	609 GCAATCTGGACCGTGTACTTGTAACTTCAGACTTCAGCATCATCTTGAGT 658	Qy	1680 TGAGGAGACACTACAGGAGTCAGCTGGCTCCAGAGGACACTTTCAGGGC 1739
Db	591 GAACTGGATGATGTCCTGTTGAGTACCATGATGTCGACAAACATCTGTTGAGT 650	Db	1665 CTTCAGAAGTGCACATTACATTACATGGGATTCAGAGAACTAATGGTCAGA 1724
Qy	669 TTGCTCTAGAATGACCGAGTCCAGCCAAATGAGATGACTC--CAGGGTGAAGAC 725	Qy	1740 AACCACTCTGTGAGGCTGGAAAGGTTCCAAAGGAAACAGTCCTATACCTACAT 1799
Db	651 CTTTATTCAAATGATGTCAGTGTGGTAAACTGGGTTAACTGGGTTAACTGGG 710	Db	1725 TAATAGACGGTCTACATGACATGGTGAAGATTATTCTACACGCCACTAATGCACT 1784
Qy	726 CACAGAGA--AGGATGGAAATCCACAGTGTGGGTTAACTGGGAAATAGTCC 782	Qy	1800 GATGGGGTGGCCTCTACTGGCTCCTGTGCCCCCTAGAGGCTCTGATGTTGGCTCTC 1859
Db	771 CTACTGGAGAACTACAGGCATCTTAAGGGTTCTCATCTGTGTAATGCTGAATCAGGCAACATCT 770	Db	1785 TGATGGGGGGCTCTCATGGCTGCTGCCCCCTGGCTCTGTCACAGCTGGGTCTC 1844
Qy	843 AACATGCCATAACAGGGGTGCTACACTTCTGAACTTCTCCCTSCAAACCTGGAC 912	Qy	1820 CTCGACCTCTGCTGGTGTACTTATGACCGAGATCAGGACCTCTGGCTCTC 1919
Db	831 AAATATCACATGTAGGGGTGGCTACATCAGAATGTTCTGGAAAGGCAAGGC 890	Db	1845 GTGTGTCCTCTGCCCTCCAGGCCACTACATGAGAAGAAACCAACCGATGCAAGGA 1904
Qy	903 GATGCGAGACAGCAGGGCTCTCTGCAACTTGTGCCAGCAACTCTTATTCAA 962	Qy	1920 CCCCTCTACACAAATTCTGAAAGGCCCTCCAGCTTATGGGTGTCAGGCCCTG 1979
Db	891 ATTCAAGCAACAAACAGGTTCTACACGGTGTGTCAGGCAACACCTTCG 950	Db	1905 TCCACCTGACACTTACCTGTCACATCAGGTTCTGACAGGCTGTCAGCT 1964
Qy	963 TAAGGAGAAACTTCCTGGCACCAGCTGACCAAACTACCTCAGAGAAAGATCTC 1022	Qy	1980 TGGTCCAGGACCAAGACACAGAACAGATCCACTCTCTGTCACATGATGTCACCTTC 2039
Db	951 GAAGAGGCCAAGAAAGATGTTAGGTGTA--AGACGACTCTCAATTTCAGATCCAG 1007	Db	1965 CGGGCTGGAGTAACAACTCAGGACCATGAGGCTTGTGTTGATGACTGCTTCTA 2024
Qy	1023 TTCTCTGTAAGTGTGCCCTGCTGACACTGACACAAAGATTTCTACACACCGGTG 1082	Qy	2040 ACCGACACTCCACAGGACGCTCACACTACACTCTCCCTGGCAACACGGTC 2099
Db	1008 TGAATGTTACAGAGGCCCTCTGTTACACAAAGACTATTCAGATCCATCTCC 1067	Db	2025 CCTGTAAGAAAGAAATCAGATTGCACTATGACTTACGACCTCTGGCTC 2084
Qy	1083 CGATGCCAACGGAGACACACATGACAAATGGCCAAACCCAAATCTGTAGGA 1142	Qy	2100 TCTGCTGGAGGCCAACGCTTACTCAAGGGTTGAARACTTCACATTTCACCT 2159
Db	1068 TGTATGAAAGAAGAAAGACACAGATGATGACAGTGTGAGAGACGCCAAATGCC 1127	Db	2085 ATTATGATGGCCCCAGCTTACCTCAGAAATACTTCATTTCAAT 2144
Qy	1143 GGACCTTGAGGGAGTGTGAGCTGCTCTGCTGCTGAGAACGCCACTGCCACCTG 1202	Qy	2160 CAGTCTCTGTTGAAACCGAGGTAGGAAATGTCGTCGACCGACAACTTCACGACCT 2219
Db	1128 GGATCTCACAGATGTTAGTGTGTTGAGTGTGCTGAGGAGAAGGGATGTCGCC 1187	Db	2145 CAGTTTGTGGCATGAGGGAAAGATGCTCTGTCACACAAATACAGACT 2204
Qy	1203 CAACCCAGGGTTCTCAAAACCAACACAGCACCTGGCAGGCCCTGCCATATGGTCTA 1262	Qy	2220 CGGATCTGGGGTGTGAGTGTGGG-----TCCTCAACATCTGAGCTTACAG 2270
		Db	2205 TACAGTAAAGAAATGTCGAGGGTCACTGATGTTGAGGATTTGTTGAGGGATTT 2264
		Qy	2271 CTCCGAGGAGTCATCTCCCTCAAGGTTGAGCTACAGGCCGAGCTTCTCACA 2330
		Db	2265 ATGCCAGTCACAAATTCTCTGAAAGTAAGGTTTCGAGCAGCTTACATCACA 2324

QY	2331	GCCGCTCACCCCTCTCTGAGCTATGGGACATACACAGATAAGCTCTGGAT	2390	FH	Key	Location/Qualifiers
Db	2325	ATCCATCATCTGGCAGATACATCATGGAGTCACAGTGTGAAACCATGAAATAT	2384	FT	CDS	1..1119 /tag= a /product= "50288 protein"
QY	2391	CACCTCCCAAGCTGAACCTTTCACCTGGAGTCCTGGATACCGGAGCTGATGGAT	2450	FT		
Db	2385	TAATAAAAGAAGATACTTCCAGTCCAAACAGCCAATACCGAGATGCAATTGATGGAT	2444	FT		
QY	2451	TTATAGTCCAAATGATGTCAGCCAGTCTGGCAGTCTGGGAGATCAACCCATCCGGGT	2510	FT		
Db	2445	TTATAGTCTCTACAGCACACATCTGTATTATGGCGATCACTGCTGAAAT	2504	XX		
QY	2511	CAGGTGCACTCCACAGAAACTGTCAGGCTGGAGGTGATTCAGTCCCAGCAAGTGCAG	2570	PN	WO200159117-A2.	
Db	2505	GAGGTGTAATCTACTAAATCTGGACAGGAGTGTGAGTCAGTCCCAGCAAGTGCAG	2564	XX		
QY	2571	TGGACACCTGATGCTCACTTCCACTTCTGAGGAGGGCTGCTGGCCACT	2630	PA	(MILL-) MILLENIUM PHARM INC.	
Db	2565	AGGTACCTGATGGGTCACTGTCATTCCTCTGGAGAGTGCTGAGCTGGCCCT	2624	XX		
QY	2631	CTGCTCAGTGGCTGACTACCATGCTATCTCAGGAGCTGTGCTGGATCCAGAAGAC	2690	PT	Glucksmann MA, Silos-Santiago I;	
Db	2625	GTGTAAGGAGCATGACTTCCATGAGATGAGGGAGGCTGCAAGAGGATTCAGAAC	2684	XX		
QY	2691	TACTAACGTTGGGAGAACCCAGCTATGCTCTGGGACATTCCTGGCAG	2750	DR	WPI: 2001-514670/56.	
Db	2685	CTGTATGTTGGAATGAACTTAAATGGCTATTAAGGATTCTTGCCTGAAAGAA	2744	DR	P-PSDB; AAB85678.	
QY	2751	AGTACCACTCTGCAAAACCATAGATTTCGCGCTAAAGGGGATCTCGAGCACCTG	2810	XX		
Db	2745	GTGCGCAACTGTGAAACGGTTGACTTGTGCTGAGGGGGCTGGAGCTT	2804	XX		
QY	2811	TACTCCATCTGTCACCCCTGACCTCTACTTGGAAAAAGATCTCAAACCTAGA	2870	CC	New seven-transmembrane protein/G-protein coupled receptor polypeptides	
Db	2805	TACGCCGTTTGTGGCTGACCGCTACTCTGGAAAGAAATCCTAAACATGGA	2864	CC	and Polynucleotides for diagnosing, treating seven-transmembrane	
QY	2871	GTACAGTACTCCAGCTGGTGAATGCTACTCTGAGACGCTGACCGAC	2930	CC	protein/receptor-related disorders and to identify modulators of	
Db	2865	ATACAAATATTCAGTTAGTAATGAGCTACTCAAAGAGTGTGACTCCGGCTGC	2924	CC	therapeutic use.	
QY	2931	TGACAGCTGCCCATCGAGGAGGAGATGTAGAGGAGGACTCT- TAACASCA 2989	XX	PS	Claim 2; Page 142; 144pp; English.	
Db	2925	AGACAGTGTGCTATCATGGAGGAGGAGTAATGAGGAGAAGTGTAAATCCATAA	2984	XX		
QY	2990	AGAATCACTCTTGGAGAGCAATCATTCATTACCTCCAGGAGCTCTGGATGATTGA	3049	CC	The invention provides isolated seven-transmembrane protein/G-protein	
Db	2985	ACAGCTCACTACTAGGAAACTCAATCTGGACCAACGAAAGAACGACATTGA	3044	CC	coupled receptor polypeptides selected from 1724, 50288, 31945 proteins.	
QY	3050	CTCACTGCCCCTGAGACATC 3070	CC	The polypeptides can be expressed by standard recombinant methodology.		
Db	3045	ATCTGTTCAACTGAAACCTC 3065	CC	Modulators of the polypeptides can be identified using a competition		
RESULT 14						
AAH70196						
ID	AAH76196	standard; cDNA; 1119 BP.				
AC	AAH76196;					
XX	29-OCT-2001	(first entry)				
XX	Human seven-transmembrane protein 50288 coding sequence.					
XX	seven-transmembrane protein; G-protein coupled receptor; GPCR; human;					
XX	anti-HIV; immunostimulant; dermatological; antiatherosclerotic; cardiot;					
XX	hepatotropic; immunosuppressive; gynecological; neuroprotective;					
XX	anti-inflammatory; anti-Parkinsonian; nephrotropic; antithyroid; hemostatic;					
XX	cerebroprotective; osteopathic; analgesic; gene therapy; nootropic; ss.					
OS	Homo sapiens.					
QY	418	GGCATTCGGTTGATGAGTGGGATGAGCTGCCCATGGCTTGGCGACCTCTCGCAC	477	QY		

Db	361	GGCACTTCGGTTGATGAGTGCTGGATGAGTCGCCATGGCTTGGCAGCCCTTCAGCCAAC	420	PA (HUMA-) HUMAN GENOME SCI INC.
QY	478	ATGGAGCTGGATGAGCAGTGGCTTCAGCAGGAACTGTGACTTCGTCAGGAACTGGTT	537	XX
Db	421	ATGGAGCTGGATGAGCAGTGGCTTCAGCAGGAACTGTGACTTCGTCAGGAACTGGTT	480	PT Ruben SM, Young PE, Baker KP;
QY	538	CCCCGGGGGACTACATCGCTTCACCGACCAATGCAAGCACACGATGACGCC 5.97	537	XX
Db	481	CCCCGGGGGACTACATCGCTTCACCGACCAATGCAAGCACACGATGACGCC 5.40	540	PT WPI; 2001-138754/14.
QY	598	GTCAACCTGAGCACTGTCACCGTGTACCTCCATACTTCCACAGCTGAGATGACTCCAGGTG 657	657	PT New nucleic acid molecule encoding a TR16 tumor necrosis factor receptor polypeptide, useful for the diagnosis and treatment of cancer, XX
Db	541	GTCAACCTGAGCACTGTCACCGTGTACCTCCACAGCTGAGATGACTCCAGGTG 600	600	PT autoimmune disorders and cardiovascular diseases -
QY	658	ATCTTGAGTTTGTCTGAGTACCGTGGCAAGCCATGAGATGACTCCAGGTG 717	717	PT apoptosis. In particular inflammatory diseases, cancers, immune and XX
Db	601	ATCTTGAGTTTGTCTGAGTACCGTGGCAAGCCATGAGATGACTCCAGGTG 660	660	PT neurodegenerative disorders may be treated.
QY	718	ATGAGACACAGAAAGGATGGAAATCCACAGTGAGCTAAATGGGAAAT 777	777	PS Disclosure: Fig 1; 286pp; English.
Db	661	ATGAGACACAGAAAGGATGGAAATCCACAGTGAGCTAAATGGGAAAT 720	720	XX
QY	778	GTCTCTATTTGAGAACACAGACAGCCCTTCAGTAGTGGACCAAAGTACCCAGGCTGCTG 837	837	CC
Db	721	GTCTCTATTTGAGAACACAGACAGCCCTTCAGTAGTGGACCAAAGTACCCAGGCTGCTG 780	780	CC factor receptor superfamily). The invention is useful treating
QY	838	GTGAGAACATTCGATACAGGGGTGCTACACTCTGAGCAGAACATCTGAGAACCT 897	897	CC diseases and disorders associated with the inhibited or increased apoptosis. In particular inflammatory diseases, cancers, immune and XX
Db	781	GTGAGAACATTCGATACAGGGGTGCTACACTCTGAGAACCT 840	840	CC neurodegenerative disorders may be treated.
QY	898	GGCACTGATGCCAGCAAGGAGGGCTCTTCGCAACTTGGCCAGCAACTT 957	957	XX
Db	841	GGCACTGATGCCAGCAAGGAGGGCTCTTCGCAACTTGGCCAGCAACTT 900	900	XX
QY	958	TCAAATAAAGGAGAACTCTTGGACACCAGTGTACCCCTGACAAATCTGAGAACAA 1017	1017	XX
Db	901	TCAAATAAAGGAGAACTCTTGGACACCAGTGTACCCCTGACAAATCTGAGAACAA 960	960	XX
QY	1018	TCT 1020		XX
Db	961	TCT 963		XX
RESULT 15				
AAF75054		Query Match 27.0%; Score 901.4; DB 22; Length 3390; Best Local Similarity 60.0%; Pred. No. 1.2e-255; Matches 1635; Conservative 0; Mismatches 1061; Indels 27; Gaps 7; Gaps QY 192 QCTTCACGCCCTGGCAAGAGCTGACTGACCTATGAGTACGACCGGGCTGACAGCACGG 251		PA
Db		Db 171 GCTCTCTCTGCGAGGAAAGTATCTGATGAAATACGGATGAGTACAGTGG 230		XX
QY		Db 252 TTCCAGGTGAGGGTGCCTGCCATACCCGGCCCTGACAGCAGGCCCTGACCC 311		XX
Db		Db 231 CTCCAGGTGAGAGTGCCTTCAATTCGACTGGACTGCTGGCTGCTGACCC 290		XX
QY		Db 312 CGTCAGGGAACCGAGTGCCTGCCTCTCCCTGCAAGGCGCCGGAGGTCTGGATGAGA 371		XX
Db		Db 291 AGTGGAGGGAAAGATGGACTCTCTGCTCTGCTCTGGAGGAGTCTGAGA 350		XX
QY		Db 372 CCAGTCATGAGCCATGGCCCTGAGGGCCCTACTCCCTGGACAGGCAATTGGTGA 431		XX
Db		Db 351 CCAGTCATGAGCTGAGTGTGAAAGGACTATTCTGGAGGAGTCTGAGTCATAATTG 410		XX
QY		Db 432 TGAGGGATGAGTGCCTCATGGCTTGGCCAGCTCTGCCACACAGGAGCTGATG 491		XX
Db		Db 411 TGAATGGGATGAAATGGCGSCAGATTTCATACTGAAACATTCATGGACACTGTG 470		XX
QY		Db 492 CAGTCCTGCTGAGTCACCGGAACTGACTCTGTCAGTGGCTCCCGGGCGA 548		XX
Db		Db 471 GGCCCTCTGAGCACAGCAGGCCAGACGGCTGCTAACACTCTCTGGATCCCTGGAA 530		XX
AC		QY 549 CTACATCGCTTCACACGGGAACTGACAGCCACACTGAGTCAGCTGCTCAACCTGA 608		XX
XX		Db 531 CTACATGAATACTGAGTACTGAGTCAGCTGCTGCTGACCTTA 590		XX
10-MAY-2001 (first entry)		QY 609 GCAATCTGGGACCGTTAACCTGAGTACTACTACATCCAGACCTCCACCATCTTGGAT 668		XX
DE		Db 591 GAAGTCAGGTTGCTCTGAGTACCTGAGTACTACATCCAGACCTCCACCATCTTGGAT 650		XX
XX		QY 669 TTTCCTTCAGATGAGCAGCAGGCCATAGAGATGACTC--CAGGGGAGGAGAC 725		XX
KW		Db 651 CTTATTCATAATGATGAGTGCAGGAGGATGGACACCAACACTGACAGTGGTAAC 710		XX
KW		QY 726 CACAGAGAA--AGATGGGAATTCCACAGTGTGAGCTAATGAGGCAATAATGTCCT 782		XX
OS		Db 711 TACAGACAATGAGATGGCTCTCTGATCTGTATGCTGAAATCAGGCACAAACATCT 770		XX
XX		QY 783 CTATGGAGACGACGGCTCTCAGTGGACAAAGTACCCAGCCCTGCTGGTGA 842		XX
12-AUG-1999;	9905-0148348.	Db 771 CTACTGGAGACGACGGCTCTAAGGGCTCTCTGATCTGTATGCTGAAATCAGGCACAAACATCT 830		XX
12-AUG-1999;	9905-0148683.	QY 843 AACATCTGGCTATAACAGGGGGCTACACTTCAGAATGCTTCCTGCAACCTGGAC 902		XX
16-AUG-1999;	9905-0148758.	Db 831 AAATATCACATGAGGGGGTGGCTACATCATGAGAATGTTCTGCAAGCCAGGAC 890		XX
17-AUG-1999;	9905-0149181.	QY 903 GTATGCAGACAAAGGGCTCTTCGCAACTTGGCCAGCCAACCTTATTCAA 962		XX
18-AUG-1999;	9905-0149453.			
19-AUG-1999;	9905-0149498.			

Db	891	ATTCAGCAACAAACCAACAGGTTCACTCACTGCAAGGNGTGTGCAAGAACCAATTCTGA	Db	1965	CGGGCCTGGAGATAAAACATCAGGACCATGGTTGTCTATAGTCACTGCTTCTCA
Qy	963	TAGGAGAAACCTCTGCCCCACAGCTGACAGAACATCTGAGAAAGATCTC	Qy	2040	ACGCACACTCCACCAAGGACTTCACACTCTCAGCTTGGCAACACCCCTCAC
Db	951	GAAGGAGCCAAGAATGTATAAGGTG	Db	2025	CCATGAAAGAAATCAGATTGTGACTATGACTTGTAGCAACCTCAGCAGTGTGGCTC
Qy	1023	TTCCTGTAACCTGCGCCACCTTGACAGACAAATCTGAGAAAGATCTC	Qy	2100	TCTGCTGGAGGCAACCTTCACTCCAAAGGTGAAACTTCATCACTTACCT
Db	1008	TCAGTGTACAGAGCGCCCTCCCTGTACCAAAAGACTATTCAGATCCATCTCAG	Db	2085	ATTAATGAAAGGCCAGCTCACCTCAAGAACAAACTTCATCTCATAT
Qy	1083	CGATGCCAACGGAGACACACTATGTCATAATGGCAACGGAAATCTTAGGA	Qy	2160	CAGTCCTGGAAACCGGGTAGGAAATGTCGTGTCAGCAGACATGTCACCT
Db	1068	TGATGAGAAGAAGACAGACAGATAATGTCAGTGTAGAGGCCAAATCTCGGGA	Db	2145	CAGTTATGGGCATGAGGGAGAAGATGGCTCTGACAGT
Qy	1143	GGACCTTGAGGGGAGTGTGAGCTGCTGCTCTGGTGAAGAACCCACTGCCCACCTG	Qy	2220	CGGATTCCTGAGGTGAGTCAGTGTGTCAGTGTGTCAGTGTGTCAGTGT
Db	1128	GGATCCTGACAGATGCAATTAGTATGAGTCGCCCTTCTGGAGAGGAGGATGTCGCC	Db	2205	TACAGTAAAGAAATAGTGTGCAAGGTGATGATTACACAAATTGGTAGGGCA
Qy	1263	CTCCAAATGG -- CTGAGCTGACCGCTGCCCTCGAGGACTAACCGCTGGGATT	Qy	2271	CTGCCAGGGAGTCATCCCGCAGGGTAGGTCAGGCTCAAGGGGGTTCTCAC
Db	1248	TTCAGATGGAAACCAAAAGAATGTAGACCATGTCAGCAGGAGGCTGCACTGGCT	Qy	2290	2331 GCGCTGTCAGCTGCTGAGCAGTATGGGGAGACACAGATGACTCTGATGGA
Qy	1320	TGATACAAATGGTGGACACGGCTGCCAGAACATGGAAACGACCGTCTGGGAT	Db	2265	ATGCCAGTCACATTATCTCTCTGAAAGTAAGGTTCCAGCAGCCTATCATCACA
Db	1368	TGATATTAATGTCATGTCATCTGTCAGTGTGAGTATCCAGAGT	Qy	2344	2385 TAATATAAAAGAAGATATGTTCCAGTTCAGTCACATGTCAGTGTGAAAT
Qy	1380	CAACTTGAGTAAAGGCAAGGCTGACAGGCTGGAGSTGGCTGGTGTGATCACAC	Qy	2445	2451 TTATAGTCCTACAGGAAACATCTGTTGAGATTAATGGGGATCACTGTCGTA
Db	1428	GGCTGGGGTTCTGACATGATGACTGTGATCTTAACATGTCATGTTAAC	Qy	2450	2511 CAGTCAGTCAGAACACTTCCCTGGAGTTCCTGCGCAGAACAGTCAGTGT
Qy	1500	TCCGAGTCGGTGTGGACAGACAGAAATAAGAGGTGGCAGAAATACATTTGCT	Db	2505	2505 GAGGTGATTCATCACTGAGGAGGAGGATTCAGTCAGTCAGCAGTCAGCCT
Db	1488	ACCAACATCTATGACTGGGACCACT -- GGGTCTGAACTAGGAAATACATTGCT	Qy	2571	2571 TGGACCTGTTGATGGCTGCAACTTCACCTCCCTGGAGACGGCGCTGCGCT
Qy	1620	CAACACTCTGGAGGAGGGAAAGGTCTCAAGGCAACAGTCCTATACCTACAT	Db	2624	2625 AGGTACCTGTGATGGCTACGTTCTCTGTTGAGGATTCAGTCAGTCAGTCAG
Db	1605	TACAATGTTGGTAAAGTCGTTGGGTGAAACAAAGAAACAGCTTACCCATATCA	Qy	2691	2691 TACTTAGGTTGGAGAACCCAGCTATGCTGTTGGCATTTCTGCTGAGGAG
Qy	1680	TCAGGAGACACTTACACGAGCTCACCTGGCTTCCAGAGGACACTTGTAGGGC	Db	2685	2685 CTGCTGAGGATGACCTAAATGGTCATTAAGGAATTCTGCTGAGAAC
Db	1665	CTTCAGAAATGCAACTTACATGAGTATGAGTATGAGTATGAGTATGAGT	Qy	2751	2751 AGTCACCTCTGCAAAACCATGATGTTCTGGTGAAGTGGCTCATCTGAGGAC
Qy	1740	AGCGAGGAATCACCAATGAGGTGGCCAAAGTCACTCTCATCAATGTCACCAAGT	Qy	2804	2745 GTGGCAACCTGTGAAACGGTGTGACTTTGGCTGAAGGGGGAGCCGGTGGAG
Db	1725	TCATAGCGGTCTCATGAGTGTGAGTATCTACAGGCACTATGAGT	Qy	2805	2805 TACTGGCTTGTGAAACGGTGTGACTTTGGCTGAAGGGGGAGCCGGTGGAG
Qy	1800	GAATGGCTGCTCTACTGCGCCCTGCCCCCTAGAGCCTGTGAGTGCTCC	Qy	2871	2871 GTACAGTACTCCAAAGCTGGTA
Db	1785	TGATGGGGTGGCTCATGCCGTCGGTCTGACAGCTGGGTTCATC	Db	2865	2865 GAGGACCATTTGAACTCTGTC
Qy	1860	CTGCACTCTGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	Search completed: March 11, 2003, 05:44:30		
Qy	1845	GGTGGCCCTGGCTCATGCCGTCGGTCTGACAGCTGGGTTCATC	Job time : 517 secs		
Qy	1920	CCCCCTAACAACTCTGAAAGCCACAGCCTATGGTGTGAGGCCCTG	1979		
Db	1905	TCCACCTGACACTACTGTGCTCATGAGTGTGACTCTGCTGATGCTG	1664		
Qy	1980	TGGTCCAGGACCAAGAACAAAGATCCACTCTGTGCTACATAATGTCAC	2439		

